SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia
KOMURIAN-PRADEL, Florence
BEDIN, Frederic
SODOYER, Mireille
OTT, Catherine
MALLET, Francois
PERRON, Herve
MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156
<141> 1999-11-02

<150> PCT/FR98/01460
<151> 1998-07-07

<150> FR/97/08816
<151> 1997-07-07

<160> 46

<170> PatentIn version 3.2

<210> 1
<211> 34
<212> DNA
<213> MSRV

<400> 1
gactcgctgc agatcgattt ttttttttt tttt 34

<210> 2
<211> 30
<212> DNA
<213> MSRV

<400> 2
gccatcaagc cacccaagaa ctcttaactt 30

<210> 3
<211> 30
<212> DNA
<213> MSRV

<400> 3
ccaatagcca gaccattata tacactaatt 30

<210> 4
<211> 310
<212> DNA
<213> MSRV

<400> 4
gcttatagaa ggacccctag tatggggtaa tcccctctgg gaaaccaagc cccagtactc 60

agcaggaaaa atagaatagg aaacctcaca aggacatact ttcctcccct ccagatggct 120

agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240

tactggacca ggccttttca aaactatcaa gaagatagtc aggggctgtg aagtgtgcca 300

aagaaataat 310

<210> 5
<211> 103
<212> PRT
<213> MSRV

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa = any amino acid

<400> 5

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys
1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
85 90 95

Glu Val Cys Gln Arg Asn Asn
100

<210> 6
<211> 635
<212> DNA
<213> MSRV

<400> 6
ccctgtatct ttaacctcct tgttaagttt gtctcttcca gaatcaaaac tgtaaaacta 60

caaattgttc ttcaaatgga gcaccagatg gagtccatga ctaagatcca ccgtggaccc 120

ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccgag 180

gaaatctcaa ctgcacaacc cctactatgc cccaattcag cgggaagcag ttagagcggt 240

catcagccaa cctccccaac agcacttggg ttttcctgtt gagaggggggg actgagagac 300

aggactagct ggatttccta ggccaacgaa gaatccctaa gcctagctgg gaaggtgact 360

gcatccacct ctaaacatgg ggcttgcaac ttagctcaca cccgaccaat cagagagctc 420

actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg 480

agagcacagc gggagggaca aggatcggga tataaaccca ggcattcgag ccggcaacgg 540

caacccccct tgggtcccct ccctttgtat gggcgctctg ttttcactct atttcactct 600

attaaatctt gcaactgaaa aaaaaaaaaa aaaaa 635

<210> 7
<211> 77
<212> PRT
<213> MSRV

<400> 7

Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys
1 5 10 15

Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser
20 25 30

Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
50 55 60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
65 70 75

<210> 8
<211> 32
<212> DNA
<213> MSRV

<400> 8
tggggttcca tttgtaagac catctgtagc tt 32

<210> 9
<211> 1481
<212> DNA
<213> MSRV

<400> 9
atggccctcc cttatcatac ttttctcttt actgttctct tacccccttt cgctctcact 60

gcacccccctc catgctgctg tacaaccagt agctcccctt accaagagtt tctatgaaga 120

acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg 240

catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt 300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt 360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat 420

agcaccccta gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc 540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta 660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga 780

atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg 840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac 900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt 960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc 1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag 1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140

caaaatcgaa gagctttaga cttgctaacc gccaaaagag ggggaacctg tttatttta 1200

ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa 1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg 1380

ttactcctct ttggaccctg tatctttaac ctccttgtta agtttgtctc ttccagaatt 1440

gaagctgtaa agctacagat ggtcttacaa atggaacccc a 1481

<210> 10
<211> 493
<212> PRT
<213> MSRV

<220>
<221> misc_feature
<222> (39)..(39)
<223> Xaa = any amino acid

<400> 10

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro
1 5 10 15

Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
20 25 30

Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
35 40 45

```
Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
    50                  55                  60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65                  70                  75                  80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
                85                  90                  95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
            100                 105                 110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
        115                 120                 125

Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
    130                 135                 140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145                 150                 155                 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
                165                 170                 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
            180                 185                 190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
        195                 200                 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
    210                 215                 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225                 230                 235                 240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
                245                 250                 255

Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
            260                 265                 270

Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
        275                 280                 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
    290                 295                 300

Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
305                 310                 315                 320
```

Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
325 330 335

Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
370 375 380

Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400

Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
420 425 430

Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
465 470 475 480

Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
485 490

<210> 11
<211> 32
<212> DNA
<213> MSRV

<400> 11
tcaaaatcga agagctttag acttgctaac cg 32

<210> 12
<211> 1329
<212> DNA
<213> MSRV

<220>
<221> misc_feature
<222> (594)..(594)
<223> n = a, g, c or t/u

<220>
<221> misc_feature
<222> (602)..(602)
<223> n = a, g, c or t/u

<220>
<221> misc_feature
<222> (1232)..(1232)
<223> n = a, g, c or t/u

<400> 12
tcaaaatcga agagctttag acttgctaac cgccaaaaga gggggaacct gtttatttt 60

aggggaagaa tgctgttagt atgttaatca atctggaatc attactgaga aagttaaaga 120

aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct 180

cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt 240

tttactcctc tttggaccct gtatcttcaa cttccttgtt aagtttgtct cttccagaat 300

tgaagctgta aagctacaaa tagttcttca aatggaaccc cagatgcagt ccatgactaa 360

aatctaccgt ggacccctgg accggcctgc tagactatgc tctgatgtta atgacattga 420

agtcacccct cccgaggaaa tctcaactgc acaaccccta ctacactcca attcagtagg 480

aagcagttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga 540

gggtggactg agagacagga ctagctggat ttcctaggct gactaagaat cccnaagcct 600

anctgggaag gtgaccgcat ccatctttaa acatggggct tgcaacttag ctcacacccg 660

accaatcaga gagctcacta aaatgctaat caggcaaaaa caggaggtaa agcaatagcc 720

aatcatctat tgcctgagag cacagcggga aggacaagga ttgggatata aactcaggca 780

ttcaagccag caacagcaac ccccttggg tcccctccca ttgtatggga gctctgtttt 840

cactctattt cactctatta aatcatgcaa ctgcactctt ctggtccgtg ttttttatgg 900

ctcaagctga gcttttgttc gccatccacc actgctgttt gccaccgtca cagacccgct 960

gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt 1020

acccattgcc actcccgatc aggctaaagg cttgccattg ttcctgcatg gctaagtgcc 1080

tgggtttgtc ctaatagaac tgaacactgg tcactgggtt ccatggttct cttccatgac 1140

ccacggcttc taatagagct ataacactca ccgcatggcc caagattcca ttccttggta 1200

tctgtgaggc caagaacccc aggtcagaga angtgaggct tgccaccatt tgggaagtgg 1260

cccactgcca ttttggtagc ggcccaccac catcttggga gctgtgggag caaggatccc 1320

ccagtaaca 1329

<210> 13
<211> 162
<212> PRT
<213> MSRV

<220>
<221> misc_feature

<222> (26)..(26)
<223> Xaa = any amino acid

<220>
<221> misc_feature
<222> (42)..(42)
<223> Xaa = any amino acid

<220>
<221> misc_feature
<222> (46)..(46)
<223> Xaa = any amino acid

<400> 13

```
Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr
1               5                  10                  15

Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly
            20                  25                  30

Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg
        35                  40                  45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
    50                  55                  60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65                  70                  75                  80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
                85                  90                  95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
            100                 105                 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
        115                 120                 125

Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
    130                 135                 140

Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
145                 150                 155                 160

Ser Ser
```

<210> 14
<211> 21
<212> DNA
<213> MSRV

<400> 14
ggcattgata gcacccatca g 21

<210> 15
<211> 21
<212> DNA
<213> MSRV

<400> 15
catgtcacca gggtggaata g 21

<210> 16
<211> 758
<212> DNA
<213> MSRV

<400> 16
ggcattgata gcacccatca gatggccaaa tcattattta ctggaccagg ccttttcaaa 60

actatcaagc agatagggcc cgtgaagcat gccaaagaaa taatcccctg ccttatcgcc 120

atgttccttc aggagaacaa agaacaggcc attacccagg ggaagactgg caactagatt 180

ttacccacat ggccaaatgt cagggatttc agcatctact agtctgggca gatactttca 240

ctggttgggt ggagtcttct ccttgtagga cagaaaagac ccaagaggta ataaaggcac 300

taatgaaata attcccagat ttggacttcc cccaggatta cagggtgaca atggccccgc 360

tttcaaggct gcagtaaccc agggagtatc ccaggtgtta ggcatacaat atcacttaca 420

ctgtgcctgg aggccacaat cctccagaaa agtcaagaaa atgaatgaaa cactcaaaga 480

tctaaaaaag ctaacccaag aaacccacat tgcatgacct gttctgttgc ctataacctt 540

actaagaatc cataactatc ccccaaaaag caggacttag cccatacgag atgctatatg 600

gatggccttt cctaaccaat gaccttgtgc ttgactgaga aatggccaac ttagttgcag 660

acatcacctc cttagccaaa tatcaacaag ttcttaaaac atcacaggga acctgtcccc 720

gagaggaggg aaaggaacta ttccaccctg gtgacatg 758

<210> 17
<211> 25
<212> DNA
<213> MSRV

<400> 17
cggacatcca aagtgatggg aaacg 25

<210> 18
<211> 26
<212> DNA
<213> MSRV

<400> 18
ggacaggaaa gtaagactga gaaggc 26

<210> 19
<211> 26
<212> DNA
<213> MSRV

<400> 19
cctagaacgt attctggaga attggg 26

<210> 20
<211> 26
<212> DNA
<213> MSRV

<400> 20
tggctctcaa tggtcaaaca tacccg 26

<210> 21
<211> 1511
<212> DNA
<213> MSRV

<400> 21
cctagaacgt attctggaga attgggacca atgtgacact cagacgctaa gaaagaaacg 60

atttatattc ttctgcagta ccgcctggcc acaatatcct cttcaaggga gagaaacctg 120

gcttcctgag ggaagtataa attataacat catcttacag ctagacctct tctgtagaaa 180

ggagggcaaa tggagtgaag tgccatatgt gcaaactttc ttttcattaa gagacaactc 240

acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacctcccta 300

ccccagcgtc ccctccccga ctccttcctc aactaataag gacccccctt taacccaaac 360

ggtccaaaag gagatagaca aaggggtaaa caatgaacca aagagtgcca atattccccg 420

attatgcccc ctccaagcag tgagaggagg agaattcggc ccagccagag tgcctgtacc 480

tttttctctc tcagacttaa agcaaattaa aatagaccta ggtaaattct cagataaccc 540

tgacggctat attgatgttt tacaagggtt aggacaatcc tttgatctga catggagaga 600

tataatgtta ctactaaatc agacactaac cccaaatgag agaagtgccg ctgtaactgc 660

agcccgagag tttggcgatc tttggtatct cagtcaggcc aacaatagga tgacaacaga 720

ggaaagaaca actcccacag gccagcaggc agttcccagt gtagaccctc attgggacac 780

agaatcagaa catggagatt ggtgccacaa acatttgcta acttgcgtgc tagaaggact 840

gaggaaaact aggaagaagc ctatgaatta ctcaatgatg tccactataa cacagggaaa 900

ggaagaaaat cttactgctt ttctggacag actaagggag gcattgagga agcatacctc 960

cctgtcacct gactctattg aaggccaact aatcttaaag gataagttta tcactcagtc 1020

agctgcagac attagaaaaa acttcaaaag tctgccttag gcccggagca gaacttagaa 1080

accctattta acttggcatc ctcagttttt tataatagag atcaggagga gcaggcgaaa 1140

cgggacaaac gggataaaaa aaaaaggggg ggtccactac tttagtcatg gccctcaggc 1200

aagcagactt tggaggctct gcaaaaggga aaagctgggc aaatcaaatg cctaataggg 1260

ctggcttcca gtgcggtcta caaggacact ttaaaaaaga ttatccaagt agaaataagc 1320

cgccccttg tccatgcccc ttacgtcaag ggaatcactg gaaggcccac tgccccaggg 1380

gatgaagata ctctgagtca gaagccatta accagatgat ccagcagcag gactgagggt 1440

gcccggggcg agcgccagcc catgccatca ccctcacaga gccccgggta tgtttgacca 1500

ttgagagcca a 1511

<210> 22
<211> 352
<212> PRT
<213> MSRV

<400> 22

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu
1 5 10 15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr
20 25 30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
290 295 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser
305 310 315 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe
325 330 335

Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro
340 345 350

<210> 23
<211> 30
<212> DNA
<213> MSRV

<400> 23
tgctggaatt cgggatccta gaacgtattc 30

<210> 24
<211> 30
<212> DNA
<213> MSRV

<400> 24
agttctgctc cgaagcttag gcagactttt 30

<210> 25
<211> 398
<212> PRT
<213> MSRV

<400> 25

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

```
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
            20                  25                  30

Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr
        35                  40                  45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
    50                  55                  60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
65                  70                  75                  80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
                85                  90                  95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
            100                 105                 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
        115                 120                 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
    130                 135                 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
145                 150                 155                 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
                165                 170                 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val
            180                 185                 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
        195                 200                 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
    210                 215                 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
225                 230                 235                 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
                245                 250                 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
            260                 265                 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
        275                 280                 285
```

```
Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His
    290                 295                 300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
305                 310                 315                 320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn
                325                 330                 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
            340                 345                 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
        355                 360                 365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu
    370                 375                 380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His
385                 390                 395
```

<210> 26
<211> 378
<212> PRT
<213> MSRV

<400> 26

```
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg
1               5                   10                  15

Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys
            20                  25                  30

Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln
        35                  40                  45

Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
    50                  55                  60

Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
65                  70                  75                  80

Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
                85                  90                  95

Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
            100                 105                 110
```

```
Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
        115                 120                 125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
    130                 135                 140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
145                 150                 155                 160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
                165                 170                 175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
            180                 185                 190

Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
        195                 200                 205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
    210                 215                 220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
225                 230                 235                 240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
                245                 250                 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
            260                 265                 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
        275                 280                 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
    290                 295                 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
305                 310                 315                 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
                325                 330                 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
            340                 345                 350

Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala
        355                 360                 365

Ala Ala Leu Glu His His His His His His
    370                 375
```

<210> 27
<211> 25
<212> DNA
<213> MSRV

<400> 27
cttggagggt gcataaccag ggaat 25

<210> 28
<211> 20
<212> DNA
<213> MSRV

<400> 28
tgtccgctgt gctcctgatc 20

<210> 29
<211> 25
<212> DNA
<213> MSRV

<400> 29
ctatgtcctt ttggactgtt tgggt 25

<210> 30
<211> 764
<212> DNA
<213> MSRV

<400> 30
tgtccgctgt gctcctgatc cagcacaggc gcccattgcc tctcccaatt gggctaaagg 60

cttgccattg ttcctgcaca gctaagtgcc tgggttcatc ctaatcgagc tgaacactag 120

tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180

ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga 240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc agcccgccac 300

tatcttggga gctctgggag caaggacccc aggtaacaat ttggtgacca cgaagggacc 360

tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa 420

atgcccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa 480

aaatgactta tattcttctg cagtaccgcc ctggccacga tatcctcttc aaggggggaga 540

aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgttttg 600

tagaaaagga ggcaaatgga gtgaagtgcc atatttacaa actttctttt cattaaaaga 660

caactcgcaa ttatgttaac agtgtgattt gtgttcctac acggaagccc tcagattcta 720

ctccccaccc ccggcatctc ccctgaatcc ctccccaact tatt 764

<210> 31
<211> 800
<212> DNA
<213> MSRV

<400> 31
tgtccgctgt gctcctgatc cagcacaggc gcccattgcc tctcccaatt gggctaaagg 60

cttgccattg ttcctgcaca gctaagtgcc tgggttcatc ctaatcgagc tgaacactag 120

tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180

ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga 240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc ggcccgccac 300

tatcttggga gctctgggag caaggacccc caggtaacaa tttggtgacc acgaagggac 360

ctgaatccgc aaccatgaag ggatctccaa agcaattgga aatgttcctc ccaaggcaaa 420

aatgccccta agatgtattc tggagaattg ggaccaatct gaccctcaga cagtaagaaa 480

aaaaatgact tatattcttc tgcagtaccg cctggccacg gatatcctct tcaaggggga 540

gaaacctggc ctcctgaggg aagtataaat tataacacca tcttacagct agacctgttt 600

tgtagaaaag gaggcaaatg gagtgaagtg ccatatttac aaactttctt ttcattaaaa 660

gacaactcgc aattatgtaa acagtgtgat ttgtgtccta caggaagccc tcagatctac 720

ctccctaccc cggcatctcc ctgactcctt ccccaactaa taaggaccca cttcagccca 780

aacagtccaa aaggacatag 800

<210> 32
<211> 65
<212> PRT
<213> MSRV

<400> 32

Pro Met Ala Ser Asn Arg Ala Ile Thr Leu Thr Ala Trp Ser Lys Ile
1 5 10 15

Pro Phe Leu Gly Ile Arg Glu Thr Lys Asn Pro Arg Ser Glu Asn Thr
20 25 30

Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser
35 40 45

Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile
50 55 60

Trp
65

<210> 33
<211> 26
<212> DNA
<213> MSRV

<400> 33
tcatgcaact gcactcttct ggtccg 26

<210> 34
<211> 28
<212> DNA
<213> MSRV

<400> 34
tcttgcacta acctccactg tccgttgg 28

<210> 35
<211> 28
<212> DNA
<213> MSRV

<400> 35
atcccccagt aacaatttgg tgaccacg 28

<210> 36
<211> 31
<212> DNA
<213> MSRV

<400> 36
tcgggtctaa gagggtactt cctttggtag g 31

<210> 37
<211> 25
<212> DNA
<213> MSRV

<400> 37
ttacgcaggt ctcagggatg agctt 25

<210> 38
<211> 33
<212> DNA
<213> MSRV

<400> 38
cggcagtagc agtcttagta tctgaagcag tta 33

<210> 39
<211> 28
<212> DNA
<213> MSRV

<400> 39
ggtacggagg gtttcatgta gttttgag 28

<210> 40
<211> 1247
<212> DNA
<213> MSRV

<220>
<221> misc_feature
<222> (1240)..(1240)
<223> n = a, g, c or t/u

<220>
<221> misc_feature
<222> (1246)..(1246)
<223> n = a, g, c or t/u

<400> 40
atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat 60

atggctagca tgactggtgg acagcaaatg ggtcggatcc tagaacgtat tctggagaat 120

tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc 180

gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat 240

tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg 300

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 360

ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact 420

ccttcctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa 480

ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgcccccc ccaagcagtg 540

agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag 600

caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta 660

caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag 720

acactaaccc caaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt 780

tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tcccacaggc 840

cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg 900

tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct 960

atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgctttt 1020

ctggacagac taagggaggc attgaggaag catacctccc tgtcacctga ctctattgaa 1080

ggccaactaa tcttaaagga taagtttatc actcagtcag ctgcagacat tagaaaaaac 1140

ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat 1200

ccggctgcta acaaagcccg aaaggaagct gagttgggtn gtggcna 1247

<210> 41
<211> 1186
<212> DNA
<213> MSRV

<400> 41
atggctagca tgactggtgg acagcaaatg ggtcggatcc tagaacgtat tctggagaat 60

tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc 120

gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat 180

tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg 240

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 300

ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact 360

ccttcctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa 420

ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgcccccc ccaagcagtg 480

agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag 540

caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta 600

caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag 660

acactaaccc caaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt 720

tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tcccacaggc 780

cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg 840

tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct 900

atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgctttt 960

ctggacagac taagggaggc attgaggaag catacctccc tgtcacctga ctctattgaa 1020

ggccaactaa tcttaaagga taagtttatc actcagtcag ctgcagacat tagaaaaaac 1080

ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat 1140

ccggctgcta acaaagcccg aaaggaagct gagttggctg gtggca 1186

<210> 42
<211> 2030
<212> DNA
<213> MSRV

<400> 42
atggccctcc cttatcatac ttttctcttt actgttctct tacccccttt cgctctcact 60

gcacccccctc catgctgctg tacaaccagt agctcccctt accaagagtt tctatgaaga 120

acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg 240

catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt 300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt 360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat 420

agcaccccta gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc 540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta 660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga 780

atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg 840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac 900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt 960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc 1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag 1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140

caaaatcgaa gagctttaga cttgctaacc gccaaaagag ggggaacctg tttatttta 1200

ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa 1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg 1380

ttactcctct ttggaccctg tatctttaac ctccttgtta agtttgtctc ttccagaatt 1440

gaagctgtaa agctacagat ggtcttacaa atggaacccc agatggagtc catgactaag 1500

atccaccgtg gacccctgga ccggcctgct agcccatgct ccgatgttaa tgacattgaa 1560

ggcacccctc ccgaggaaat ctcaactgca caacccctac tatgccccaa ttcagcggga 1620

agcagttaga gcggtcatca gccaacctcc ccaacagcac ttgggttttc ctgttgagag 1680

gggggactga gagacaggac tagctggatt tcctaggcca acgaagaatc cctaagccta 1740

gctgggaagg tgactgcatc cacctctaaa catggggctt gcaacttagc tcacacccga 1800

ccaatcagag agctcactaa aatgctaatt aggcaaaaat aggaggtaaa gaaatagcca 1860

atcatctatt gcctgagagc acagcgggag ggacaaggat cgggatataa acccaggcat 1920

tcgagccggc aacggcaacc ccctttgggt cccctccctt tgtatgggcg ctctgttttc 1980

actctatttc actctattaa atcttgcaac tgaaaaaaaa aaaaaaaaaa 2030

<210> 43
<211> 2055
<212> DNA
<213> MSRV

<400> 43
cagcaacccc ctttgggtcc cctcccattg tatgggagct ctgttttcac tctatttcac 60

tctattaaat catgcaactg cactcttctg gtccgtgttt tttatggctc aagctgagct 120

tttgttcgcc atccaccact gctgtttgcc accgtcacag acccgctgct gacttccatc 180

cctttggatc cagcagagtg tccgctgtgc tcctgatcca gcacaggcgc ccattgcctc 240

tcccaattgg gctaaaggct tgccattgtt cctgcacagc taagtgcctg ggttcatcct 300

aatcgagctg aacactagtc actgggttcc acggttctct tccatgaccc atggcttcta 360

atagagctat aacactcact gcatggtcca agattccatt ccttggaatc cgtgagacca 420

agaaccccag gtcagagaac acaaggcttg ccaccatgtt ggaagcagcc caccaccatt 480

ttggaagcag cccgccacta tcttgggagc tctgggagca aggaccccag gtaacaattt 540

ggtgaccacg aagggacctg aatccgcaac catgaaggga tctccaaagc aatgggaaac 600

gttcccccg aggcaaaaat gcccctagaa cgtattctgg agaattggga ccaatgtgac 660

actcagacgc taagaaagaa acgatttata ttcttctgca gtaccgcctg gccacaatat 720

cctcttcaag ggagagaaac ctggcttcct gagggaagta taaattataa catcatctta 780

cagctagacc tcttctgtag aaaggagggc aaatggagtg aagtgccata tgtgcaaact 840

ttcttttcat taagagacaa ctcacaatta tgtaaaaagt gtggtttatg ccctacagga 900

agccctcaga gtccacctcc ctaccccagc gtcccctccc cgactccttc ctcaactaat 960

aaggaccccc ctttaaccca aacggtccaa aaggagatag acaaaggggt aaacaatgaa 1020

ccaaagagtg ccaatattcc ccgattatgc cccctccaag cagtgagagg aggagaattc 1080

ggcccagcca gagtgcctgt acctttttct ctctcagact taaagcaaat taaaatagac 1140

ctaggtaaat tctcagataa ccctgacggc tatattgatg ttttacaagg gttaggacaa 1200

tcctttgatc tgacatggag agatataatg ttactactaa atcagacact aaccccaaat 1260

gagagaagtg ccgctgtaac tgcagcccga gagtttggcg atctttggta tctcagtcag 1320

gccaacaata ggatgacaac agaggaaaga acaactccca caggccagca ggcagttccc 1380

agtgtagacc ctcattggga cacagaatca gaacatggag attggtgcca caaacatttg 1440

ctaacttgcg tgctagaagg actgaggaaa actaggaaga agcctatgaa ttactcaatg 1500

atgtccacta taacacaggg aaaggaagaa aatcttactg cttttctgga cagactaagg 1560

gaggcattga ggaagcatac ctccctgtca cctgactcta ttgaaggcca actaatctta 1620

aaggataagt ttatcactca gtcagctgca gacattagaa aaaaacttca aaagtccgtc 1680

ttaggctcgg aacaaaactt agaaacccta ttgaacttgg caacctcggt tttttataat 1740

agagatcagg aggagcaggc agaatgggac aaatgggata aaaaaaaaag ggccaccgct 1800

ttagtcatgg ccctcaggca agcggacttt ggaggctctg gaaaagggaa aagctgggca 1860

aataggaagc ctaatagggc ttgcttccag tgcggtctac aaggacactt taaaaaagat 1920

tgtccaaata gaaataagcc gccccccttgt ccatgcccct tacgtcaagg gaatcactgg 1980

aaggcccact gccccagggg atcaagatac tctgagtcag aagccattaa ccagatgatc 2040

cagcagcagg actga 2055

<210> 44
<211> 1197
<212> DNA
<213> MSRV

<400> 44
ggacccgtag tatggggtaa tcccctccgg gaaaccaagc cccagtactc agaagaagaa 60

atagaatggg gaacctcacg aggacatggt ttcctcccct caggatggct agccactgaa 120

gaaggaaaaa tacttttgct ggcagctaac caatggaaat tacttaaaac ccttcagcaa 180

accttccact taggcattga tagcacccat cagatagcca aatcattatt tactggacca 240

ggccttttca aaactatcaa gcagatagtc agggcctgtg aagtgtgcca aagaaataat 300

cccctgcctt atcgccaagc tccttcagga gaacaaagaa caggcaatta cccaagagaa 360

gactggcaac tagattttat ccacatgcca aaatcacagg gatttcagtg tctactagtc 420

tgggtagata ctttcactgg ttgggcagag gccttcccct gtaggacaga aaagttccaa 480

gaggtaataa aggcactagt tcatgaagta attcccagat tcggacttcc ctgaggctta 540

cagagtgaca atggtcctgc tttcaaggcc acagtaaccc agggagtatc ccaggcgtta 600

ggtatagaat atcacttaca ctgcacctag aggccacaat cctcagggaa ggttgagaaa 660

atgaaaacac tcaaacgaca tctaaacaag ctaacccagg aaacccacct cgcatggtct 720

gctctgttgt ctatagcctt actaagaatc caaaactctc cccaaaaggc aggacttagc 780

ccatacagaa tgctgtatgg acggtccttc ctaaccaatg accttctgct tgaccaagag 840

atggccaact tagttgcaga catcacctcc ttagccaaat atcaacaagt tcttaaaaca 900

ttacaaggag cctgtccccg agaggaggga aaagaaatat tccaccctgg tgtcatggta 960

ttagtcaagt cccttccctc taattcccca tccctagaca catcctgggg aggaccctac 1020

ccagtcattt tatctatccc aactgcggtt aaagtggctg gagtggagtc ttggatacat 1080

cacactcgaa tcaaaccctg gatactgccg aaggaacccg aaaatccagg ggacaacgct 1140

agctatttct ttgaacctct agaggatctg tgcctgctct tcaagcaaca accgtga 1197

<210> 45
<211> 1718
<212> DNA
<213> MSRV

<400> 45
gagaatagca gcataagttg gctggcagaa gtagggaaag acagcaagaa gtaaagaaaa 60

aaaggagaaa gtcagagaaa gaaaaaaaga gaggaagaaa caaagaagaa cttgaagaga 120

gaaagaagta gtaaagaaaa aacagtatac cctattcctt taaaagccag ggtaaatttc 180

tgtctaccta gccaaggcat attcttctta tgtggaacat caacctatat ctgcctcccc 240

actaactgga caggcaccag aaccttagtc tttctaagtc ccaacattaa cattgcccca 300

ggaaatcaga ccctattggt acctgtcaaa gctaaagtcc gtcagtgcag agccatacaa 360

ctaatatccc tatttatagg gttaggaatg gctactgcta caggaactgg aatagccggt 420

ttatctactt cattatccta ctaccataca ctctcaaaga atttctcaga cagtttgcaa 480

gaaataatga aatctattct tactttacaa tcccaattag actctttggc agcaatgact 540

ctccaaaacc gccgaggccc acacctcctc actgctgaga aaggaggact ctgcaccttc 600

ttaggggaag agtgttgttt ttacactaac cagtcaggga tagtacgaga tgccacctgg 660

catttacagg aaagggcttc tgatatcaga caatgccttt caaactctta taccaacctc 720

tggagttggg caacatggct tcttccattt ctaggtccca tggcagccat cttgctgtta 780

ctcacctttg ggccctgtat ttttaagctt cttgtcaaat ttgtttcctc taggatcgaa 840

gccatcaagc tacagatggt cttacaaatg gaaccccaaa tgagttcaac taacaacttc 900

taccaaggac ccctggaacg atccactggc acttccacta gcctagagat tcccctctgg 960

aagacactac aactgcaggg ccccttcttt gcccctatcc agcaggaagt agctagagcg 1020

gtcatcggcc aaattcccaa cagcagttgg ggtgtcctgt ttagaggggg gattgaagag 1080

tgacagcctg ctggcagcct cacagccctc gttggatctc agtgcctcct cagccttggt 1140

gcccactctg gccgtgcttg aggagccctt cagcctgcca ctgcactgtg ggagcctctt 1200

tctgggctgg acaaggccgg agccagctcc ctcagcttgc agggaggtat ggagggagag 1260

atgcaggcgg gaaccagggc tgcgcatggc gcttgcgggc cagcatgagt tccaggtggg 1320

cgtgggctcg gcgggcccca cactcgggca gtgaggggct tagcacctgg gccagacaga 1380

tgctgtgctc aacttcttcg ctgggcctta gctgccttcc ccgtggggca gggctacggg 1440

aacatgcagc ctgcccatgc ttgagccccc caccccgccg tgggttcytg cacagcccaa 1500

gcttcccgga caagcaccac cccttatcca cggtgcccag tcccatcaac cacccaaggg 1560

ttgaggagtg cgggcacaca gcgcgggatt ggcaggcagt tccacttgcg gccttggtgc 1620

gggatccact gcgtgaagcc agctgggctc ctgagtctgg tggggacttg gagaatcttt 1680

atgtctagct aagggattgt aaatacacca atcagcac 1718

<210> 46
<211> 1628
<212> DNA
<213> MSRV

<400> 46
atggccctcc cttatcatac ttttctcttt actgttctct taccccctttt cgctctcact 60

gcacccccctc catgctgctg tacaaccagt agctcccctt accaagagtt tctatgaaga 120

acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg 240

catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt 300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt 360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat 420

agcaccccta gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc 540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta 660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga 780

atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg 840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac 900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt 960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc 1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag 1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140

caaaatcgaa gagctttaga cttgctaacc gccaaaagag ggggaacctg tttattttta 1200

ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa 1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg 1380

ttactcctct ttggaccctg tatctttaac ctccttgtta agtttgtctc ttccagaatc 1440

aaaactgtaa aactacaaat tgttcttcaa atggagcacc agatggagtc catgactaag 1500

atccaccgtg gacccctgga ccggcctgct agcccatgct ccgatgttaa tgacattgaa 1560

ggcacccctc ccgaggaaat ctcaactgca caacccctac tatgccccaa ttcagcggga 1620

agcagtta 1628